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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/679,643

DATE: 07/29/2004

TIME: 14:21:31

Input Set : N:\Crf3\RULE60\09679643.raw
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1 <110> APPLICANT: Foster, Timothy J.
 2 McDevitt, Damien L.
 3 <120> TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
 4 <130> FILE REFERENCE: 05344.105011
 5 <140> CURRENT APPLICATION NUMBER: US/09/679,643
 6 <141> CURRENT FILING DATE: 2000-10-05
 7 <150> PRIOR APPLICATION NUMBER: US/08/293,728
 8 <151> PRIOR FILING DATE: 1994-08-22
 9 <160> NUMBER OF SEQ ID NOS: 20
 10 <170> SOFTWARE: PatentIn Ver. 2.0
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 3498
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Staphylococcus aureus
 16 <220> FEATURE:
 17 <221> NAME/KEY: CDS
 18 <222> LOCATION: (301)..(3099)
 19 <400> SEQUENCE: 1
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 22 attcttaaaa tagcaataaaa taaaatgttt gtttagtaaag tattattgtg gataataaaa 180
 23 tatcgataca aattaattgc tataatgcaa ttttagtgta taattccatt aacagagatt 240
 24 aaatatatct taaagggtat atagttataa taaaatgact tttaaaaaag agggataaaa 300
 25 atg aat atg aag aaa aaa gaa aaa cac gca att cgg aaa aaa tcg att 348
 26 Met Asn Met Lys Lys Glu Lys His Ala Ile Arg Lys Lys Ser Ile
 27 1 5 10 15
 28 ggc gtg gct tca gtg ctt gta ggt acg tta atc ggt ttt gga cta ctc 396
 29 Gly Val Ala Ser Val Leu Val Gly Thr Leu Ile Gly Phe Gly Leu Leu
 30 20 25 30
 31 agc agt aaa gaa gca gat gca agt gaa aat agt gtt acg caa tct gat 444
 32 Ser Ser Lys Glu Ala Asp Ala Ser Glu Asn Ser Val Thr Gln Ser Asp
 33 35 40 45
 34 agc gca agt aac gaa agc aaa agt aat gat tca agt agc gtt agt gct 492
 35 Ser Ala Ser Asn Glu Ser Asn Asp Ser Ser Val Ser Ala
 36 50 55 60
 37 gca cct aaa aca gac gac aca aac gtg agt gat act aaa aca tcg tca 540
 38 Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser
 39 65 70 75 80
 40 aac act aat aat ggc gaa acg agt gtg gcg caa aat cca gca caa cag 588
 41 Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln
 42 85 90 95
 43 gaa acg aca caa tca tca aca aat gca act acg gaa gaa acg ccg 636
 44 Glu Thr Thr Gln Ser Ser Thr Asn Ala Thr Glu Glu Thr Pro

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49	gca aca act caa tca agc aat aca aat gcg gag gaa tta gtg aat caa			732
50	Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln			
51	130	135	140	
52	aca agt aat gaa acg act ttt aat gat act aat aca gta tca tct gta			780
53	Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val			
54	145	150	155	160
55	aat tca cct caa aat tct aca aat gcg gaa aat gtt tca aca acg caa			828
56	Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Gln			
57	165	170	175	
58	gat act tca act gaa gca aca cct tca aac aat gaa tca gct cca cag			876
59	Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln			
60	180	185	190	
61	agt aca gat gca agt aat aaa gat gta gtt aat caa gcg gtt aat aca			924
62	Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr			
63	195	200	205	
64	agt gcg cct aga atg aga gca ttt agt tta gcg gca gta gct gca gat			972
65	Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp			
66	210	215	220	
67	gca ccg gca gct ggc aca gat att acg aat cag ttg acg aat gtg aca			1020
68	Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr			
69	225	230	235	240
70	gtt ggt att gac tct ggt acg act gtg tat ccg cac caa gca ggt tat			1068
71	Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr			
72	245	250	255	
73	gtc aaa ctg aat tat ggt ttt tca gtg cct aat tct gct gtt aaa ggt			1116
74	Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly			
75	260	265	270	
76	gac aca ttc aaa ata act gta cct aaa gaa tta aac tta aat ggt gta			1164
77	Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val			
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79	act tca act gct aaa gtg cca cca att atg gct gga gat caa gta ttg			1212
80	Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu			
81	290	295	300	
82	gca aat ggt gta atc gat agt gat ggt aat gtt att tat aca ttt aca			1260
83	Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr			
84	305	310	315	320
85	gac tat gta aat act aaa gat gat gta aaa gca act ttg acc atg ccc			1308
86	Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro			
87	325	330	335	
88	gct tat att gac cct gaa aat gtt aaa aag aca ggt aat gtg aca ttg			1356
89	Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu			
90	340	345	350	
91	gct act ggc ata ggt agt aca aca gca aac aaa aca gta tta gta gat			1404
92	Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val Asp			
93	355	360	365	

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94	tat gaa aaa tat ggt aag ttt tat aac tta tct att aaa ggt aca att	1452
95	Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile Lys Gly Thr Ile	
96	370 375 380	
97	gac caa atc gat aaa aca aat aat acg tat cgt cag aca att tat gtc	1500
98	Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val	
99	385 390 395 400	
100	aat cca agt gga gat aac gtt att gcg ccg gtt tta aca ggt aat tta	1548
101	Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu	
102	405 410 415	
103	aaa cca aat acg gat agt aat gca tta ata gat cag caa aat aca agt	1596
104	Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser	
105	420 425 430	
106	att aaa gta tat aaa gta gat aat gca gct gat tta tct gaa agt tac	1644
107	Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr	
108	435 440 445	
109	ttt gtg aat cca gaa aac ttt gag gat gtc act aat agt gtg aat att	1692
110	Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile	
111	450 455 460	
112	aca ttc cca aat cca aat caa tat aaa gta gag ttt aat acg cct gat	1740
113	Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp	
114	465 470 475 480	
115	gat caa att aca aca ccg tat ata gta gtt gtt aat ggt cat att gat	1788
116	Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp	
117	485 490 495	
118	ccg aat agc aaa ggt gat tta gct tta cgt tca act tta tat ggg tat	1836
119	Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr	
120	500 505 510	
121	aac tcg aat ata att tgg cgc tct atg tca tgg gac aac gta gca	1884
122	Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala	
123	515 520 525	
124	ttt aat aac gga tca ggt tct ggt gac ggt atc gat aaa cca gtt gtt	1932
125	Phe Asn Asn Gly Ser Gly Asp Gly Ile Asp Lys Pro Val Val	
126	530 535 540	
127	cct gaa caa cct gat gag cct ggt gaa att gaa cca att cca gag gat	1980
128	Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu Asp	
129	545 550 555 560	
130	tca gat tct gac cca ggt tca gat tct ggc agc gat tct aat tca gat	2028
131	Ser Asp Ser Asp Pro Gly Ser Asp Ser Gly Ser Asp Ser Asn Ser Asp	
132	565 570 575	
133	agc ggt tca gat tcg ggt agt gat tct aca tca gat agt ggt tca gat	2076
134	Ser Gly Ser Asp Ser Gly Ser Asp Ser Thr Ser Asp Ser Gly Ser Asp	
135	580 585 590	
136	tca gcg agt gat tca gat tca gca agt gat tca gac tca gcg agt gat	2124
137	Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp	
138	595 600 605	
139	tca gat tca gca agc gat tcc gac tca gcg agc gat tcc gac tca gac	2172
140	Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp	
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142	aat gac tcg gat tca gat agc gat tct gac tca gac agt gac tca gat	2220

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146	Ser	Asp															
147	645				650			655									
148	tca	gat	tca	gat	agc	gat	tca	gat	agc	gat	tca	gat	tcc	gac		2316	
149	Ser	Asp															
150	660		665			670											
151	agt	gat	tcc	gac	tca	gac	agc	gat	tct	gac	tcc	gac	agt	gat	tcc	gac	2364
152	Ser	Asp															
153	675		680			685											
154	tca	gac	agc	gat	tca	gat	tcc	gac	agt	gat	tcc	gac	tca	gat	agc	gat	2412
155	Ser	Asp															
156	690		695			700											
157	tcc	gac	tca	gat	agc	gac	tca	gat	agc	gat	tca	gat	tca	gac		2460	
158	Ser	Asp															
159	705		710			715										720	
160	agc	gat	tca	gat	tca	gat	agc	gat	tca	gat	tcc	gac	agt	gac	tca	gat	2508
161	Ser	Asp															
162	725			730			735										
163	tcc	gac	agt	gac	tcg	gat	tca	gat	agc	gat	tcc	gac	agt	gac		2556	
164	Ser	Asp															
165	740		745			750											
166	tca	gat	tcc	gac	agt	gac	tca	gac	tcg	agt	gat	tcg	gat	tca	gcg		2604
167	Ser	Asp	Ser	Ala													
168	755		760			765											
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170	Ser	Asp															
171	770		775			780											
172	tca	gat	agc	gac	tca	gac	tcg	gat	agc	gac	tcg	gat	tca	gat	agc	gat	2700
173	Ser	Asp															
174	785		790			795										800	
175	tcg	gac	tca	gat	agc	gat	tca	gaa	tca	gac	agc	gat	tca	gaa	tca	gac	2748
176	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
177	805			810			815										
178	agc	gat	tca	gat	tca	gac	agc	gac	tca	gac	agt	gac	tca	gat	tca	gat	2796
179	Ser	Asp															
180	820		825			830											
181	agt	gac	tcg	gat	tca	gac	tcg	agt	gat	tca	ggt	agt	gac	tcc	gat		2844
182	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Asp	
183	835		840			845											
184	tca	tca	agt	gat	tcc	gac	tca	gaa	agt	gat	tca	aat	agc	gat	tcc	gag	2892
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186	850		855			860											
187	tca	ggt	tct	aac	aat	aat	gta	ggt	ccg	cct	aat	tca	cct	aaa	aat	ggt	2940
188	Ser	Gly	Ser	Asn	Asn	Asn	Val	Val	Pro	Pro	Asn	Ser	Pro	Lys	Asn	Gly	
189	865			870			875								880		
190	act	aat	gct	tct	aat	aaa	aat	gag	gct	aaa	aat	gat	agt	aaa	gaa	cca	ttt
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 197 Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg Lys Lys Glu
 198 915 920 925
 199 aat aaa gat aag aaa taagtaataa tgatattaaa ttaatcatat gattcatgaa 3139
 200 Asn Lys Asp Lys Lys
 201 930
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 203 attaataatt aattcatcaa cagtttaatta tttaaaaag gtagatgtta tataatttgg 3259
 204 cttggcgaaa aaatagggtg taaggttagt tggtaattag gggaaattaa ggagaaaata 3319
 205 cagttgaaaa ataaattgtc agttttatca ttgggagcat tatgtgtatc acaaatttgg 3379
 206 gaaagtaatc gtgcgagtgc agtggttct ggggagaaga atccatatgt atctgagtcg 3439
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 219 35 40 45
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 221 50 55 60
 222 Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser
 223 65 70 75 80
 224 Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln
 225 85 90 95
 226 Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro
 227 100 105 110
 228 Val Thr Gly Glu Ala Thr Thr Thr Asn Gln Ala Asn Thr Pro
 229 115 120 125
 230 Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln
 231 130 135 140
 232 Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val
 233 145 150 155 160
 234 Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln
 235 165 170 175
 236 Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln
 237 180 185 190
 238 Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr
 239 195 200 205
 240 Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp
 241 210 215 220

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